

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 HUMAN SERVICES
 Schneerson, Rachel
 Leppla, Stephen H.
 Robbins, John B.
 Shiloach, Joseph
 Kubler-Kielb, Joanna
 Liu, Darrell
 Majadly, Fathy

<120> GAMMA PGA CONJUGATES FOR ELICITING IMMUNE RESPONSES DIRECTED
 AGAINST BACILLI

<130> 4239-68226-01

<150> US 60/476,598

<151> 2003-06-05

<160> 3

<170> PatentIn version 3.2

<210> 1

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Basic peptide derived from HIV-1 Tat protein.

<400> 1

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
 1 5 10

<210> 2

<211> 2295

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1)..(2292)

<400> 2

atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata	48
Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile	
1 5 10 15	
tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa	96
Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys	
20 25 30	
cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta	144
Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu	

35	40	45	
cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val 50 55 60			192
acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu 65 70 75 80			240
aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly 85 90 95			288
ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala 100 105 110			336
gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys 115 120 125			384
gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln 130 135 140			432
ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp 145 150 155 160			480
ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser 165 170 175			528
agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser 180 185 190			576
aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp 195 200 205			624
aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp 210 215 220			672
gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His 225 230 235 240			720
gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser 245 250 255			768
acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile 260 265 270			816
gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr			864

275	280	285	
ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu 290 295 300			912
gat caa tcc aca cag aat act gat agt caa acg aga aca ata agt aaa Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys 305 310 315 320			960
aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala 325 330 335			1008
gaa gtg cat gcg tgc ttc ttt gat att ggt ggg agt gta tct gca gga Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly 340 345 350			1056
ttt agt aat tcg aat tca agt acg gtc gca att gat cat tca cta tct Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser 355 360 365			1104
cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala 370 375 380			1152
gat aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr 385 390 395 400			1200
gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa Ala Pro Ile Tyr Asn Val Leu Pro Thr Ser Leu Val Leu Gly Lys 405 410 415			1248
aat caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln 420 425 430			1296
ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile 435 440 445			1344
gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn 450 455 460			1392
tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp 465 470 475 480			1440
acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly 485 490 495			1488
aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg caa Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln 500 505 510			1536
att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta aat Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn			1584

515	520	525	
ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu 530 535 540			1632
acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe 545 550 555 560			1680
gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile 565 570 575			1728
acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys 580 585 590			1776
aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp 595 600 605			1824
aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg 610 615 620			1872
ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val 625 630 635 640			1920
ggt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu 645 650 655			1968
ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile 660 665 670			2016
gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg 675 680 685			2064
tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe 690 695 700			2112
ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn 705 710 715 720			2160
ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile 725 730 735			2208
att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys 740 745 750			2256
att tta atc ttt tct aaa aaa ggc tat gag ata gga taa Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly			2295

755

760

<210> 3
 <211> 764
 <212> PRT
 <213> Bacillus anthracis

<400> 3

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
 1 5 10 15

Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
 20 25 30

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
 35 40 45

Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
 50 55 60

Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
 65 70 75 80

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
 85 90 95

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
 100 105 110

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
 115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
 130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
 145 150 155 160

Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
 165 170 175

Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
 180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
 195 200 205

Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
 210 215 220

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
 225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
 245 250 255

Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
 260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
 275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
 290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
 305 310 315 320

Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
 325 330 335

Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
 340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
 355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
 370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
 385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
 405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
 420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
 435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
 450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
 465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
 485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
 500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
 515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
 530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
 545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
 565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
 580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
 595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
 610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
 625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
 645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
 660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
 675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755 760